

GenScore version 4.5
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OM protein - protein search, using sw model

Run on: March 12, 2002, 12:49:01 : Search time 22.94 seconds

(without alignments)
43,206 Million cell updates/sec

Title: US-09-801-784-36

Perfect score: 50

Sequence: 1 PSAAVALTISP 10

Scoring table:

BLOSUM62
Gapop 10.0 / Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 68

Listing first 45 summaries

Database :

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	88.0	171	2	A41467
2	40	80.0	170	1	YOEBC1
3	40	80.0	170	1	R56617
4	38	76.0	2344	2	S64740
5	36	72.0	234	2	S22134
6	36	72.0	326	2	S27901
7	36	72.0	326	2	T17743
8	36	72.0	377	1	MPNZP2
9	36	72.0	427	2	T41257
10	35	70.0	537	2	S62749
11	35	70.0	251	2	A55523
12	35	70.0	260	2	S72748
13	35	70.0	374	1	DEHUAS
14	35	70.0	374	1	A56436
15	35	70.0	424	2	T34663
16	35	70.0	444	2	S64912
17	35	70.0	486	2	S74319
18	35	70.0	804	2	H75549
19	35	70.0	963	2	S45167
20	35	70.0	2344	2	S55399
21	34	68.0	331	2	G75035
22	34	68.0	350	2	T40466
23	34	68.0	460	2	B82549
24	34	68.0	540	1	OYHDCR
25	34	68.0	570	2	T37314
26	34	68.0	610	2	T35797
27	34	68.0	1877	2	T40550
28	34	68.0	2016	2	A38195
29	33	66.0	115	2	S75392

40	33	66.0	154	2	CR2971
41	33	66.0	161	2	T52409
42	33	66.0	199	2	T52410
43	33	66.0	201	2	T52408
44	33	66.0	212	2	T01605
45	33	66.0	225	2	H75548
46	33	66.0	310	2	T43158
47	33	66.0	314	2	T43299
48	33	66.0	469	1	MPNZ1A
49	33	66.0	475	1	S62658
40	33	66.0	482	1	MPNZ41
41	33	66.0	409	2	E70643
42	33	66.0	441	2	S54744
43	33	66.0	547	1	ERADP2
44	33	66.0	561	2	T46845
45	33	66.0	664	1	H32243

ALIGNMENTS

RESULT 1
A41467
Limbrial protein csaA - Escherichia coli plasmid pEU405
N:Alternate names: CSI plus major subunit
C:Species: Escherichia coli
C:Date: 30-Jun-1992 #sequence revision 30-Jun-1992 #text change 26-Aug-1999
C:Accession: A41467; S19003
R:Peretz-Gasal, J.; Swaffley, J.S.; Strota, J.R.
Interf. Immun. 58: 3594-3600, 1990
A:Title: Gene encoding the major subunit of CSI plus of human enterococcal plasmid Escherichia coli
A:Reference number: A41467; MIMD:9104170
A:Accession: A41467
A:Molecule type: DNA
A:Residues: 1-171 - PER.
A:Cross-references: GRM:7148; GR:M58550; NID:0414573; JLN:AAA550; JLN:0414574
A:Journal: J.M.A.M.; van Vliet, A.H.M.; Williams, G.A.; van der Zant, E.A.M.; Baasstra
FEMS Microbiol. Lett. 80: 265-270, 1991
A:Title: Analysis of the first two genes of the CSI limbrial operon in human enterococci
A:Reference number: S19092
A:Accession: S19093
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-171 - JON.
A:Cross-references: EMBL:X62879; NID:041169; PIRN:CAA467; JLN:0414571
A:Geneticist:
C:Species: csaA
A:Gene: csaA
A:Genome: Plasmid
C:Superfamily: csaA limbrial protein

Query Match 88.0% Score 44 DB 2: Length 171
Host local similarity 80.0% Pred. No. 0.24
Matches 8: Conservative 2: Mismatches 0: Indels 0: Gaps 0

QY 1 PSAAVALTISP 10
LB 49 PSAAVALTISP 58

RESULT 2
CPAL limbrial protein precursor - Escherichia coli
N:Alternate names: CPAL plimr; colonization factor antigen 1 (CPA1)
C:Species: Escherichia coli
C:Date: 14-Nov-1983 #sequence revision 30-Jun-1991 #text change 15-Nov-1996
C:Accession: A0589; A03495; A43841
R:Kajalaidon, T.R.; Evans, D.S.; So, M.; Lee, C.H.
Interf. Immun. 57: 1126-1130, 1989
A:Title: Molecular cloning and nucleotide sequence of the colonization factor antigen
A:Reference number: A0589; MIMD:89174309
A:Accession: A0589
A:Molecule type: DNA

Conserved hypochlorite
of binding in 11 Dmp-
to be cognate binding
to be cognate binding
phylogenetic A2944
conserved hypochlorite
probable cAMP binding
prolactin-like binding
maternal protein
d-oxidized dehydrogen
matrix protein - S
probable 199K prot
transcription factor
605K 110K protein
K- transport 100 A1
phosphatransferase

S27901
 Site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) (vial1) Chloroella
 N:Alternate names: DNA adenine methyltransferase (vial1)
 C:Species: Chloroella virus PhCV-1
 C>Date: 09-Jun-1994 #sequence_revision 10 Nov-1995 #text_change 05-May-2000
 C:Accession: S54442; S27901
 R:Zhang, Y.; Nelson, M.; Nietfeldt, J.W.; Huthank, B.E.; van Etten, J.L.
 Nucleic Acids Res. 20, 5451-5456, 1992
 A>Title: Characterization of chloroella virus PhCV-1 (vial1) restriction and modification
 A:Reference number: S54442; MUID:93065201
 A:Accession: S54442
 A:Molecule type: DNA
 A:Residues: 1-126 <EET>
 A:Cross-references: EMBL:M86639; NID:4323316; PID:4323317
 C:Superfamily: site-specific methyltransferase (adenine-specific) Nid111
 C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 72.0%; Score 36; DB 2; Length 126;
 Best Local Similarity 70.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 PSAVALIYSP 10
 1 1 1 1 1 1 1
 DB 95 PGFVITLYSP 104

RESULT 7
 117743
 Site-specific DNA-methyltransferase (adenine-specific) (EC 2.1.1.72) - Chloroella virus 1
 C:Species: Chloroella virus PhCV-1
 C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 05-May-2000
 C:Accession: T17743
 R:Graves, M.V.; Van Etten, J.L.
 submitted to the EMBL data library, May 1999
 A:Reference number: Z18806
 A:Accession: T17743
 A>Status: preliminary; translated from GH/EMBL/MBR1
 A:Molecule type: DNA
 A:Residues: 1-126 <GRA>
 A:Cross-references: EMBL:042580; NID:4402896; PID:AA096619.1
 C:Genetics:
 A:Note: A251R
 C:Superfamily: site-specific methyltransferase (adenine-specific) Nid111
 C:Keywords: methyltransferase; S-adenosylmethionine

Query Match 72.0%; Score 36; DB 2; Length 126;
 Best Local Similarity 70.0%; Pred. No. 17;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

1 PSAVALIYSP 10
 1 1 1 1 1 1 1
 DB 95 PGFVITLYSP 104

RESULT 8
 MENT2
 matrix protein - parainfluenza virus type 2
 C:Species: parainfluenza virus type 2
 C>Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 16-Jul-1999
 C:Accession: A16421; S16661
 R:Kakano, M.; Bando, H.; Ohgimoto, S.; Okamoto, K.; Kondo, K.; Isumidome, M.; Nishio, M.;
 Virology 179, 857-861, 1990
 A>Title: Complete nucleotide sequence of the matrix gene of human parainfluenza type 2
 A:Reference number: A16421; MUID:91049454
 A:Accession: A16421
 A:Molecule type: genomic RNA
 A:Residues: 1-377 <KAM>
 A:Cross-references: GH:M62744; NID:4342740; PID:AAA46662.1; FID:4342741
 R:Kawano, M.; Okamoto, K.; Bando, H.; Kondo, K.; Isumidome, M.; Komada, H.; Nishio, M.;
 Nucleic Acids Res. 19, 2739-2746, 1991
 A>Title: Characterizations of the human parainfluenza type 2 virus gene encoding the F

A:Reference number: S16659; MUID:91252221
 A:Accession: S16661
 A:Molecule type: genomic RNA
 A:Residues: 1-377 <RAW>
 A:Cross-references: EMBL:X57559; NID:961985; PID:CAA40745.1; FID:961986
 A:Experimental source: strain Toshiba
 C:Genetics:
 A:Gene: M
 C:Superfamily: parainfluenza virus matrix protein
 C:Keywords: matrix protein

Query Match 72.0%; Score 36; DB 1; Length 477;
 Best Local Similarity 60.0%; Pred. No. 20;
 Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

1 PSAVALIYSP 10
 1 1 1 1 1 1 1
 DB 170 PFEVSTIYSP 179

RESULT 9
 141257
 hypobiotic protease Spoz285.11 - Histon yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T41257
 R:Seeger, K.; Bartis, D.; Lynn, M.; Rajandream, M.A.; Bartis, R.;
 submitted to the EMBL data library, September 1998
 A:Reference number: Z21981
 A:Accession: T41257
 A>Status: preliminary; translated from GH/EMBL/MBR1
 A:Molecule type: DNA
 A:Residues: 1-427 <SEE>
 A:Cross-references: EMBL:AF031545; PID:CAZ0850.1; GSPDB:G0000067; S138; SPOZ285.11
 A:Experimental source: strain 972H-; cosmid c285
 C:Genetics:
 A:Gene: SPOB:SP03285.11
 A:Map position: 4
 A:Inserts: 36/4

Query Match 72.0%; Score 36; DB 2; Length 427;
 Best Local Similarity 70.0%; Pred. No. 22;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

1 PSAVALIYSP 10
 1 1 1 1 1 1 1
 DB 203 PSAVIMYSP 212

RESULT 10
 S62749
 Alpha X protein (allele 4) - bracket fungus (Schizophyllum commune)
 C:Species: Schizophyllum commune
 C>Date: 24-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 23-Jul-2000
 C:Accession: S62749
 R:Matton, A.L.; Bartholomew, K.A.; Wu, J.; Yano, H.; Novotny, C.F.; Murtha, R.;
 Curr. Genet. 29, 143-149, 1996
 A>Title: The Alpha mating type locus of Schizophyllum commune: structure and function
 A:Reference number: S62749; MUID:96418876
 A:Accession: S62749
 A>Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-537 <MAK>
 A:Cross-references: EMBL:U01943; NID:4537622; PID:AAA41498.1; FID:4537623
 A:Note: The nucleotide sequence was submitted to the EMBL data library, August 1994
 C:Genetics:
 A:Inserts: 21/4
 C:Superfamily: Alpha X protein
 Query Match 72.0%; Score 36; DB 2; Length 537;

best local similarity 60.0%; Score 45; Pos 2; Length 241;
 Matched 6; Conserved 4; Mis-matches 2; Indels 0; Gaps 0;
 07 1 OSAAVATVSP 10
 11 111111
 08 172 OSAAVATVSP 101

RESULT 11
 Accession: A55624
 Hypothetical protein (bipid 6' region) Pseudomonas sp. (strain KKS102)
 c) Species: Pseudomonas sp.
 c) Date: 25 Aug 1993 #sequence revision 25 Aug 1993 #text change 08 Oct 1999
 c) Accession: A55624
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: A55624; MIMD:94179104
 c) Accession: A55624
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-251 - KKK
 c) Cross reference: GenBank: MIMD:941840; EMBL:AA04111.1; FID:4400460; FID:441769

Query Match 70.0%; Score 45; Pos 2; Length 241;
 best local similarity 60.0%; Score 20;
 Matched 6; Conserved 4; Mis-matches 2; Indels 0; Gaps 0;
 07 1 OSAAVATVSP 10
 11 111111
 08 172 OSAAVATVSP 101

RESULT 12
 Accession: S2748
 Hypothetical protein Mycobacterium leprae
 c) Species: Mycobacterium leprae
 c) Date: 19 Mar 1997 #sequence revision 25 Apr 1997 #text change 24 Mar 2001
 c) Accession: S2748
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: S2748
 c) Accession: S2748
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

Query Match 70.0%; Score 45; Pos 2; Length 241;
 best local similarity 60.0%; Score 21;
 Matched 7; Conserved 4; Mis-matches 2; Indels 0; Gaps 0;
 07 1 OSAAVATVSP 10
 11 111111
 08 172 OSAAVATVSP 101

RESULT 13
 Accession: S2748
 Hypothetical protein Mycobacterium leprae
 c) Species: Mycobacterium leprae
 c) Date: 19 Mar 1997 #sequence revision 25 Apr 1997 #text change 24 Mar 2001
 c) Accession: S2748
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: S2748
 c) Accession: S2748
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

Active Expression and Kinetic characterization of recombinant human stomach alcohol
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

Active Expression and Kinetic characterization of recombinant human stomach alcohol
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

Active Expression and Kinetic characterization of recombinant human stomach alcohol
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

Active Expression and Kinetic characterization of recombinant human stomach alcohol
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Keyword: Y.; Nucleic Ac.; Kinetics; K.; Kinetics; M.; Yano; K.; Takai; M.
 c) Referral: 176; 169; 1994; 1994
 c) Title: Identification of the bipid gene encoding ferredoxin reductase involved in bipid
 c) Reference number: A55678; MIMD:95181314
 c) Accession: A55678
 c) Status: preliminary
 c) Molecular type: DNA
 c) CDS: 1-260 - SMT
 c) Cross reference: EMBL:U00011; FID:446607; FID:AAAT7112.1; FID:446647

A:Pathway: alcohol degradation
 C:Function: <RDH>
 A:Description: catalyzes the oxidation of retinol to retinal by NAD-
 A:Pathway: retinoic acid biosynthesis
 A:Note: abundant in stomach, eye, skin, thymus, and ovary
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F:2-374/Product: alcohol dehydrogenase 7 *status experimental <MAT>
 F:12-365/Domain: long-chain alcohol dehydrogenase homology <LADR>
 F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Gly) (in mature form) *status predicted
 F:47-68,174/Binding site: zinc, catalytic (Cys, His, Cys) *status experimental
 F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) *status experimental

Query Match 70.0% Score 45: DB 1: Length 474:
 Best Local Similarity 70.0% Pred. No. 41:
 Matches 7: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 296 PSAAKMLITDP 305

RESULT 14

A56436
 A:Alcohol dehydrogenase (EC 1.1.1.1) IV - mouse
 N:Alternate names: class IV alcohol dehydrogenase am elating class IV alcohol dehydrogenase
 N:Contains: retinol dehydrogenase (EC 1.1.1.105)
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Jul-1995 *sequence_revision 21 Jul-1995 *text change 11 Jun-1999
 C:Accession: A56436
 R:Zygmunt-Knight, M.; Ang, H.L.; Foglio, M.H.; Dinesley, G.
 J. Biol. Chem. 270, 10868-10877, 1995
 A:Title: Cloning of the mouse class IV alcohol dehydrogenase (retinol dehydrogenase) cDN
 A:Reference number: A56436; MIM:95256259
 A:Accession: A56436
 A:Molecule type: mRNA
 A:Residues: 1-374 <ZD>
 A:Cross-references: GB:020257; NID:q897584; PUD:AAA76745.1; PII:q847985
 C:Genetics:
 A:Gene: Adh-3
 C:Complex: homodimer
 C:Function: <ADH>
 A:Description: catalyzes the oxidation of primary and secondary alcohols to aldehydes an
 A:Pathway: alcohol degradation
 C:Function: <RDH>
 A:Description: catalyzes the oxidation of retinol to retinal by NAD-
 A:Pathway: retinoic acid biosynthesis
 A:Note: retinoic acid regulates epithelial cell differentiation
 A:Note: abundant in stomach, eye, skin, thymus, and ovary
 C:Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology
 C:Keywords: acetylated amino end; alcohol metabolism; dimer; metalloprotein; NAD; oxidoreductase
 F:2-374/Product: alcohol dehydrogenase IV *status predicted <MAT>
 F:12-365/Domain: long-chain alcohol dehydrogenase homology <LADR>
 F:194-223/Region: beta-alpha-beta NAD nucleotide-binding fold
 F:2/Modified site: acetylated amino end (Gly) (in mature form) *status predicted
 F:47-68,174/Binding site: zinc, catalytic (Cys, His, Cys) *status predicted
 F:98,101,104,112/Binding site: zinc, noncatalytic (Cys) *status predicted

Query Match 70.0% Score 45: DB 1: Length 474:
 Best Local Similarity 70.0% Pred. No. 41:
 Matches 7: Conservative 0: Mismatches 4: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 296 PSAAKMLITDP 305

RESULT 15

133663

Hydroxylated protein W04B5.3 - Caenorhabditis elegans
 C:Species: Caenorhabditis elegans
 C:Date: 29-Oct-1999 *sequence_revision 29-Oct-1999 *text change 29-Oct-1999
 C:Accession: U34664
 R:Smith, A.; Gibson, A.
 Submitted to the EMBL Data Library, October 1998
 A:Description: The sequence of C. elegans cosmid W04B5.
 A:Reference number: Z21485
 A:Accession: U34664
 A:Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-424 <SM>
 A:Cross-references: EMBL:AF100305; PUD:MAC68916.1; CSIRO:CM00021; CESP:W04B5.3
 A:Experimental source: strain Bristol N2; clone W04B5
 C:Genetics:
 A:Gene: CESP:W04B5.3
 A:Map position: 4
 A:Features: 7/3: 64/3: 102/3: 124/3: 144/3: 198/3: 277/3: 301/3: 417/3: 499/3

Query Match 70.0% Score 45: DB 2: Length 424:
 Best Local Similarity 60.0% Pred. No. 45:
 Matches 6: Conservative 4: Mismatches 1: Indels 0: Gaps 0:

1 PSAAVATYSP 10
 111 111 1
 282 PSAAVATYSP 291

Search completed: March 12, 2002, 12:49:02
 Job time: 267 sec

Tue Mar 12 14:28:00 2002

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